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Research Article

Enhanced Brain Tumor Detection using Adaptive Preprocessing and Hybrid Deep Learning Techniques

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ABSTRACT

Neurological and brain cancers represent major global health issues, with MRI serving as a vital diagnostic tool. However, interpreting MRI images manually is often slow and prone to inconsistency. This study presents a sophisticated framework for detecting brain tumors using Dynamic Contrast-Enhanced MRI (DCE-MRI). The framework integrates advanced preprocessing and hybrid deep learning techniques to enhance performance. Adaptive multi-scale Gaussian filtering is used initially to reduce noise and enhance picture quality. Following the identification of the most relevant features using Recursive Feature Elimination with Cross-Validation (RFECV), Levy Flight Particle Swarm Optimization (LFPSO) is used to optimize feature extraction. Convolutional neural networks (CNNs) and long short-term memory networks (LSTMs) are combined in a hybrid deep learning model to accomplish the classification, which successfully captures both temporal and spatial patterns. This methodology offers notable improvements in detection accuracy and processing speed, showcasing its potential for clinical use and better patient outcomes.

Keywords: MRI, brain tumor detection, adaptive preprocessing, hybrid deep learning, DCE-MRI, CNN, LSTM.

INTRODUCTION

The Accurate brain tumor classification [1] is essential for prompt medical diagnosis and treatment. MRI, a vital non-invasive imaging technique, provides high-contrast images essential for tumor detection. This study explores two advanced approaches: Transfer learning with EfficientNets categorizes tumors into glioma, meningioma, and pituitary tumors, achieving up to 99.06% accuracy and 98.79% F1-score. Additionally, the Exponential Deer Hunting Optimization-based Shepard Convolutional Neural Network (ExpDHO-based ShCNN) and ExpDHO-based Deep CNN [2] are utilized for detection and classification. This method includes noise reduction, image segmentation, and augmentation, with sensitivity, specificity, and accuracy values of 0.919, 0.939, and 0.939, respectively, demonstrating excellent performance.

Image segmentation [3] is vital yet challenging for diagnosing brain tumors, which affect essential CNS functions. MRI is a standard tool for detecting these tumors, but classification can be difficult. Two novel techniques are presented in this paper [4]: one for tumor segmentation using the Adaptive Flying Squirrel Algorithm and another for MRI image classification using an Adaptive Fuzzy Deep Neural Network with Frog Leap Optimization. Implemented in MATLAB, the first method achieves 99.6% accuracy, 99.9% sensitivity, and 99.8% specificity. Additionally, DeepTumorNet, a GoogLeNet-based hybrid deep learning model, provides exceptional classification for glioma, meningioma, and pituitary tumors, with 99.67% accuracy and 100% recall.

In medical imaging, the categorization of brain tumors [5] is essential for efficient diagnosis and care. An Optimized Hybrid Deep Neural Network (OHDNN) that improves brain tumor detection in two key stages is presented in this paper: pre-processing and classification. Initially, MRI images are improved through enhancement and noise reduction. The Adaptive Rider Optimization (ARO) technique is used to improve the

OHDNN [6], which combines Convolutional Neural Networks (CNN) for feature extraction with Long Short-Term Memory (LSTM) networks for classification. The approach achieves up to 97.5% accuracy. Additionally, the paper addresses MRI image segmentation, highlighting preprocessing methods, CNN-based segmentation, and the impact of strength normalization and data augmentation on accuracy.

A novel approach [7] that uses advanced segmentation algorithms on MRI images to identify brain tumors. Leveraging recent advancements in deep learning, to improve tumor detection, the method makes use of inception modules and convolutional neural networks. Automated segmentation improves speed and consistency despite data variations. Significant improvements in dice score, sensitivity, and specificity are shown by new deep neural network designs [8], such as MI-Unet and depth-wise separable MI-Unet. The depth-wise separable hybrid Unet performs highest. Adaptive Kernel Fuzzy C-Means (AKFCM) is used for segmentation and Stationary Wavelet Packet Transform (SWPT) is used for feature extraction in the suggested hybrid deep learning technique, enhanced by a CNN-LSTM model. Evaluated in MATLAB, the method demonstrates high accuracy and precision.

The Accurate brain tumor classification [9] is vital for early diagnosis and treatment. This study proposes an advanced AI-based framework combining Vision Transformer (ViT) and deep neural networks for enhanced classification. The framework includes preprocessing, data normalization, and feature extraction using Haralick features and local binary patterns. Optimized Convolutional Neural Networks (CNN) [10] capture local details, while ViT manages long-range dependencies. A machine learning model is used to classify, weight, and fuse the features. Evaluated on multiple MRI datasets, this ensemble approach shows improved performance. Additionally, the paper introduces a Deep Convolutional Neural Network (DCNN) optimized with Harris Hawks Optimization (HHO) and Grey Wolf Optimization (GWO), achieving 97% accuracy with enhanced speed and reduced memory usage.

These research focuses on improving brain tumor detection through an integrated approach that combines advanced preprocessing, feature selection, feature extraction, and classification techniques for Dynamic Contrast-Enhanced MRI (DCE-MRI). To improve image quality by reducing noise and increasing contrast, it uses adaptive multi-scale Gaussian filtering, which is vital for precise feature extraction. Levy Flight Particle Swarm Optimization (LFPSO) efficiently extracts important features from the MRI images, while Recursive Feature Elimination with Cross-Validation (RFECV) selects the optimal features. Convolutional neural networks (CNNs) and long short-term memory (LSTM) networks are combined in a hybrid deep learning model for categorization to capture both temporal and spatial information. The proposed method is benchmarked against existing approaches, showing notable improvements in tumor detection accuracy, sensitivity, and processing efficiency.

The following is the format of the essay's subsequent sections: A short summary of some of the research in the areas of preprocessing, feature extraction, feature selection, and disease classification is provided in Section 2. The proposed method for the CNN-LSTM system is described in detail in Section 3. A summary of the results of the experimental performance analysis is given in Section 4. Finally, a summary of the results is provided in Section 5.

RELATED WORK

In [11], Nazir et al (2021) reviews and critically evaluates new research on the use of deep learning methods with MRI images for brain tumor classification and detection. Aimed at deep learning experts interested in applying their skills to brain tumor research, the study begins with a summary of previous work in this area. Then, in a comparison table, it offers a thorough assessment of deep learning techniques put out in academic publications between 2015 and 2020. In the context of brain tumor detection and classification, the conclusion outlines the advantages and disadvantages of deep neural networks.

In [12], Qasem et al (2019) proposes a MRI and CT brain scans for brain tumor detection, favoring MRI for its lower risk. We applied the watershed segmentation technique, with the methodology divided into preprocessing, foreground computation using watershed, and feature extraction for machine learning algorithms. The approach was tested on a large dataset, and in identifying brain cancers, the K-NN classification system produced results with a beneficial level of accuracy.

In [13], Solanki et al (2023) proposes a various method for detecting brain cancer and tumors, providing an assessment matrix for different systems and datasets. Brain tumor morphology, accessible datasets, augmentation methods, feature extraction, and classification utilizing Deep Learning (DL), Transfer Learning (TL), and Machine Learning (ML) models are all covered to a certain extent. The paper also consolidates information on tumor identification, detailing the benefits, limitations, advancements, and future trends in the field.

In [14], Khairandish et al (2020) assessed according to the performance, suggested model, dataset, and algorithm type. In these experiments, the accuracy scores varied from 79% to 97.7%. In descending order of frequency, the most used algorithms were CNN, KNN, C-means, and RF. While the methods demonstrated promising results, the accuracy for brain tumor detection still requires improvement. Additionally, developing software applications could enhance practical solutions for real-world cases.

In [15], Alsaif et al (2022) emphasizes on models such as ResNet, AlexNet, and VGG while providing a thorough analysis of various CNN architectures. Then, it presents a successful method for MRI dataset-based brain tumor identification that makes use of CNN and data augmentation approaches. Considering the superior deep architectural design and excellent detection accuracy, the assessment measures show that the suggested approach significantly advances previous research.

In [16], Jabbar et al (2023) provides a comprehensive review of various CNN architectures, focusing particular emphasis on models like VGG, AlexNet, and ResNet. Then, utilizing CNN and data augmentation techniques, it offers a successful approach for brain tumor identification using MRI datasets. According to assessment results, the suggested method offers increases in both detection accuracy and deep architectural design, hence making substantial progress over earlier studies.

In [17], Rajan and Sundar (2019) effectively segments brain tumors by combining active contour by level set, K-means clustering, and fuzzy C-means (KMFCM). This approach enhances segmentation, edge detection, and intensity, facilitating easy tumor detection. Active contour with level set method ensures precise segmentation. The number of white and black pixels determines how well the system performs, detected tumor area, and processing time. It effectively handles complex segmentation tasks with minimal execution time. Additionally, to ascertain the values of the similarity index, sensitivity, specificity, and accuracy, tumor dimensions are examined. To help physicians with diagnosis and treatment planning, tumor volume is also computed.

In [18], Thayumanavan and Ramasamy (2021) proposed framework for tumor classification involves several stages, including feature extraction, segmentation, classification, and preprocessing. The first input consists of T1-weighted MRI brain images. To improve the extraction of aberrant brain tissues in low contrast and precisely identify the margins of afflicted regions, a median filter is used for skull stripping optimization in MRI images. The Histogram of Oriented Gradients (HOG), which focuses on texture and shape characteristics, and the Discrete Wavelet Transform (DWT) are used for feature extraction. Machine learning methods such as Random Forest Classifier (RFC), Support Vector Machine (SVM), and Decision Tree (DT) are then used for classification, with performance evaluated through sensitivity, specificity, and accuracy metrics.

In [19], Vankdothu et al (2022) suggests combining a CNN with an LSTM network, where the LSTMs improve the CNNs' ability to extract features. The combined LSTM-CNN architecture performs better than conventional CNN models in image classification tasks. The suggested approach outperforms earlier CNN and RNN models in terms of accuracy, according to experiments done using a Kaggle dataset of 3,264 MRI scans, which is divided into 2,870 images for training and 394 for testing. The results indicate a significant improvement in classification performance using the LSTM-CNN hybrid approach.

In [20], Sajid et al (2019) presents a deep learning technique for brain tumor segmentation that makes use of many MRI modalities. Using a patch-based methodology, the suggested hybrid convolutional neural network (CNN), considering both local and contextual information to predict output labels. To address overfitting, dropout regularization and batch normalization are employed, while a two-phase training process tackles data imbalance. The method includes preprocessing steps for image normalization and bias field correction, followed by a CNN feed-forward pass and removing small false positives close to the skull using post-processing. Utilizing the BRATS 2013 dataset for validation, the approach outperforms current methods with dice scores, sensitivity, and specificity of 0.86, 0.86, and 0.91, respectively.

PROPOSED METHODOLOGY

This research proposes a hybrid deep learning approach for brain tumor identification and classification. The proposed method consists of three main steps: preprocessing, feature selection, and classification. The general block diagram of the suggested system is shown in Fig. 1.

3.1 Input dataset collection

The BraTS (Brain Tumor Segmentation) [21] Challenge offers datasets focused on brain tumor analysis, primarily using structural MRI modalities like T1, T1Gd, T2, and FLAIR. Some versions also include Dynamic

Contrast-Enhanced MRI (DCE-MRI) sequences, which provide additional detail by capturing contrast agent dynamics, crucial for tumor vascular characterization.

These datasets are meticulously annotated with tumor sub-regions, aiding in model training for tumor detection and classification. Researchers can benchmark their algorithms using metrics like Dice score, sensitivity, and specificity. BraTS datasets are vital for developing robust, accurate diagnostic tools in brain tumor analysis.

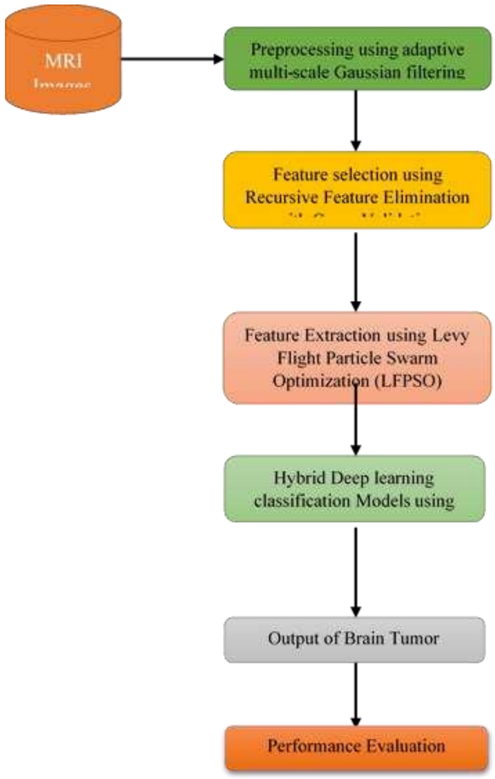

Fig 1 overall block diagram of Brain Tumor Prediction

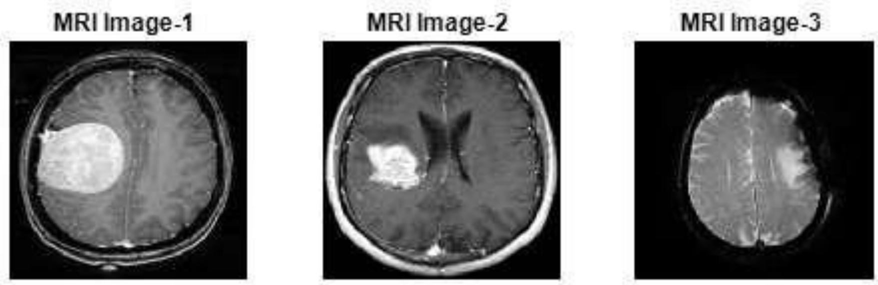

Fig 2. Input Images

3.2 Pre-processing using adaptive multi-scale Gaussian filtering Algorithm

The adaptive multi-scale Gaussian filtering algorithm approach was used in this investigation [22] is employed for pre-processing to improves detection accuracy and speed, achieving an accuracy, sensitivity, specificity, Dice Similarity Coefficient with processing times averaging with seconds.

Based on this paper, the Adaptive Multi-Scale Gaussian Filtering (AMGF) is an image processing technique that dynamically adjusts the Gaussian filter's variance (σ^2)based on local image characteristics, enhancing image quality by addressing challenges like noise suppression and edge preservation. The two-dimensional Gaussian filter is expressed in equation (1):

$$G\ (x, y) = \frac{1}{2\pi\sigma^2} \exp\left(-\frac{(x^2+y^2)}{2\sigma^2}\right) \tag{1}$$

where $G\ (x,\ y)$ represents the Gaussian filter function, σ^2 is the variance, and x and y are the pixel coordinates. Typically, values below 5% of the kernel's maximum value are excluded to calculate the filter kernel size.

Traditional Gaussian filtering, while effective at noise suppression, can blur important features and cause issues like edge displacement, vanishing edges, and phantom edges, especially where pixel intensity changes abruptly.

AMGF addresses these issues through two main strategies:

- Multi-Scale Filtering: The image is pre-processed using Gaussian filters with different variances, capturing both fine and broad features. This allows for a synthesis of results that balances noise suppression with edge preservation.
- Adaptive Variance: The filter variance is adjusted based on local image characteristics (e.g., noise level, edge type), ensuring that, in accordance with their particular needs, various image components are smoothed differently.

Mathematically, Gaussian filtering of a signal $F(x)$ denoted as $F_z(x)$ can be expressed as equation (2):

$$F_z(x) = F(x) + \frac{\sigma^2}{2}F''(x) + higher\_order\ terms \quad (2)$$

Where $F''(x)$ is the second derivative of $F(x)$.

The adaptive variance $\sigma^2(x,y)$ is often defined as the equation (3):

$$\sigma^2(x,y) = \frac{1}{F(x,y)} \quad (3)$$

where $F(x,\ y)$ is the pixel brightness (intensity). This approach adapts the filter to the specific needs of each region, preserving fine details while reducing noise in more homogeneous areas.

A more advanced method minimizes assuming that the variance does not vary much across pixels, the mean square error. Minimizing the error $E\ (\sigma)$, which is defined as follows, yields the ideal filter variance:

$$E\ (\sigma) = ||G * F - F||^2 + \lambda\ ||\nabla\sigma||^2\ \ \| \quad (4)$$

where G is the Gaussian filter, F is the image, $*$ denotes convolution, and the variance field's smoothness is controlled by the regularization value λ.

Medical imaging is one area where AMGF is very useful, such as MRI, where it enhances critical structures while effectively suppressing noise. This makes it valuable for tasks like edge detection, segmentation, and feature extraction.

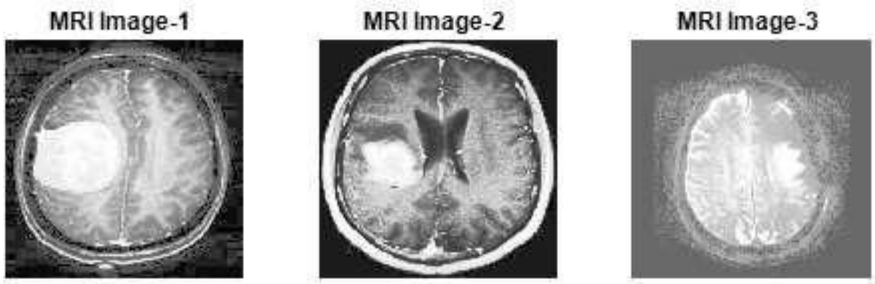

Fig 3. Pre-processed Images

Algorithm 1: AMGF algorithm

1. Pre-process the image using Gaussian filters with varying σ^2 values (multi-scale filtering).
2. Compute the local image characteristics (e.g., intensity, contrast).
3. Adaptively adjust the Gaussian filter variance $\sigma^2(x,y)$ based on local characteristics.
4. Apply the adaptive Gaussian filter to the image.

5. Minimize the error $E(\sigma)$ to find the optimal filter variance for each pixel.
6. Combine the results of the different scales to produce the final enhanced image.

The Adaptive Multi-Scale Gaussian Filtering (AMGF) algorithm [22] proves to be a robust pre-processing method, particularly in medical imaging, where it significantly enhances image quality by dynamically adjusting the Gaussian filter's variance based on local characteristics. This adaptability ensures effective noise suppression while preserving crucial image details, especially at edges where pixel intensity changes sharply. The AMGF algorithm's ability to optimize filter variance for each pixel contributes to improved detection accuracy and processing speed, making it a useful tool for uses such edge detection, segmentation, and feature extraction.

3.3 Feature selection using Recursive Feature Elimination with Cross-Validation (RFECV) algorithm

The RFECV technique is used in this study to select features from the provided datasets. For selecting the most relevant features for intrusion detection, RFECV [23], a wrapper approach for feature selection, uses a machine learning algorithm. It improves resilience by finding out the optimum amount of features that optimize model performance by combining cross-validation and recursive feature reduction.

In RFECV, features that do not increase classification accuracy are repeatedly eliminated once each feature has been evaluated by a classification model. As described in Algorithm 2, the process starts with the complete set of features and gradually eliminates those they eventually determine the most useful feature subset, but do not add to classification accuracy. For this research, RFECV was implemented using the Decision Tree model (DT-RFECV) with a 10-fold cross-validation strategy and Stratified Fold splitting to maintain the class distribution. Ten folds of the same size were created from the dataset.

During the recursive elimination process, to assess how feature removal affects model performance, the accuracy measure is calculated at each iteration. Each iteration calculates the accuracy metric to evaluate the impact of feature removal on model performance. The feature subset that results in the highest overall accuracy is selected as optimal.

Following the elimination procedure, 10-fold cross-validation is used to confirm the chosen feature set. With each fold serving as the validation set and the remaining folds being utilized for training, the Decision Tree model is trained and assessed 10 times. To determine how effectively the model generalizes to new data and how resilient it is, accuracy metrics are computed. A comprehensive evaluation of performance is given by the accuracy measures' average and standard deviation throughout the 10 iterations.

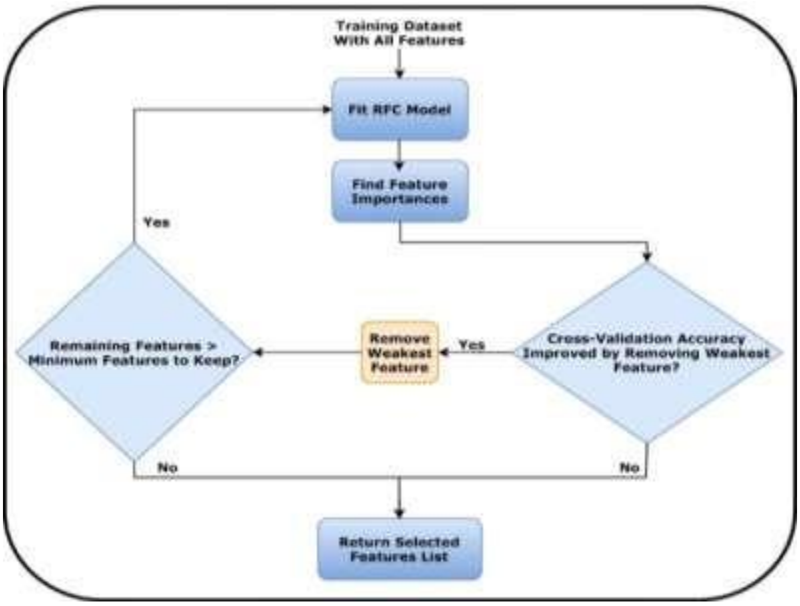

Fig 2 RFECV flowchart model diagram

Algorithm 2: RFECV algorithm

Input: Training dataset X

Output: Ranked features

1. For each feature in the dataset X:
2. For k=1 to 10 (where k is the number of cross-validation folds):
   - Using the StratifiedKFold technique, randomly divide the dataset X into 10 equal subgroups.
   - Nine subsets should be used as the training set, and one subset should be used as the validation set.
   - Use the training data to train the classification model.
   - Using the validation data, determine the model's prediction accuracy.
   - Determine each feature's significance based on the model's assessment.
   - Update the training data and eliminate the l least significant characteristics.
3. Identify the feature subset FS that achieves the highest prediction accuracy.
4. If FS has the highest prediction accuracy:
5. Mark FS as the selected features.
6. Return the ranked list of selected features.

Algorithm 2 explains that RFECV [24], the use of RFECV facilitated a thorough evaluation of feature importance and contributed to developing an increasingly precise and generalizable model. The selected feature set demonstrated improved performance and better generalization to unseen data, reinforcing the effectiveness of RFECV in enhancing feature selection for intrusion detection. Overall, RFECV proves to be a robust and reliable technique for optimizing feature sets, leading to more accurate and reliable models for intrusion detection and similar applications.

3.4 Feature Extraction using Levy Flight Particle Swarm Optimization (LFPSO)

In this concept, LFPSO [25] is an advanced optimization algorithm that enhances the traditional Particle Swarm Optimization (PSO) by integrating Levy flight, which improves the exploration capabilities of the swarm. This combination is particularly useful in complex optimization problems such as brain tumor detection, where it can optimize feature selection, parameter tuning, and other critical tasks.

LFPSO incorporates the Levy flight mechanism into the PSO framework. Levy flight is a random walk strategy characterized by heavy-tailed distributions, which allows for better global exploration and helps avoid local optima. By leveraging these properties, LFPSO enhances the performance of PSO in complex search spaces. In LFPSO, every particle has a velocity V_i and a location X_i. Equations (5) and (6) are used to update each particle's location and velocity in the manner shown below:

$$V_i(t+1) = \omega \,.\, V_i(t) + c_1 \,.\, r_1 . (\rho_{best,i} - X_i) + c_2 \,.\, r_2 . (g_{best} - X_i) \tag{5}$$

$$X_i(t+1) = X_i(t) + V_i(t+1) \tag{6}$$

Here, ω is the inertia weight, c_1 *and* $c_2$are acceleration coefficients, r_1 *and* $r_2$are random numbers in [0,1], $\rho_{best,i}$ represents particle i optimal position, while g_{best} represents the optimal position globally.

The Levy flight mechanism modifies the standard particle movement. A random vector **L** drawn from a Levy distribution is used to update the particle's position in equation (7) as follows:

$$X_{new} = X + \alpha \, . \, \mathbf{L} \tag{7}$$

In this, **L** represents the Levy flight step size, which is typically generated from a Levy distribution in equation (8):

$$\mathbf{L}(\lambda) = \frac{\boldsymbol{u}}{|\boldsymbol{v}|\mathbf{1}/\boldsymbol{\lambda}} \tag{8}$$

where u and v are random variables drawn from normal distributions, and λ is the Levy flight exponent, usually set to 1.5.

The LFPSO algorithm begins with the initialization of a swarm of particles with random positions and velocities, and parameters such as inertia weight, acceleration coefficients, and Levy flight parameters are set. Each particle's fitness is evaluated based on the objective function, such as accuracy in brain tumor detection. The algorithm then updates each particle's personal best and global best positions based on fitness evaluations.

The Levy flight update step involves generating a random step size from the Levy distribution and updating each particle's position in equ (9):

$$X_i(t+1) = X_i(t) + \alpha \, . \, \mathbf{L} \tag{9}$$

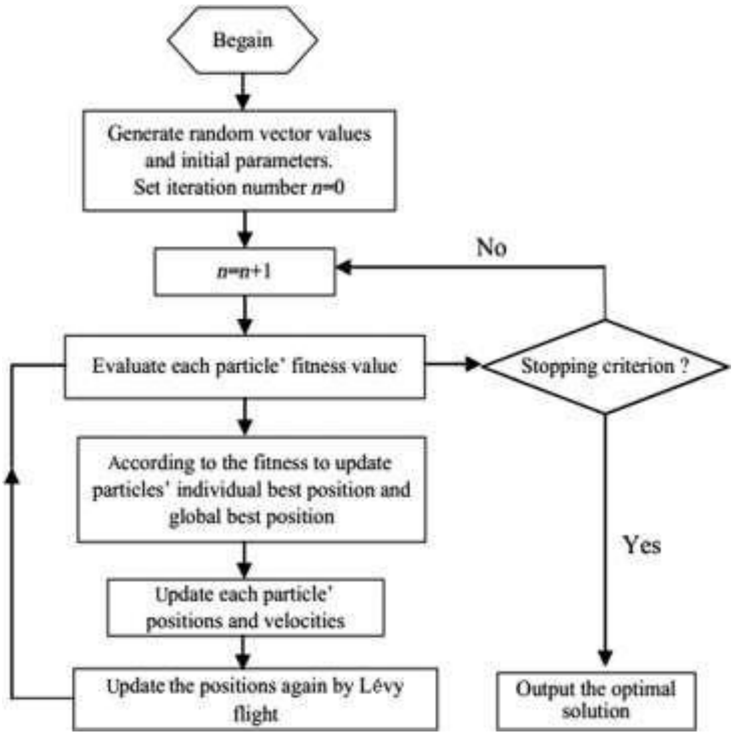

Fig 3 Flowchart of the Lévy particle swarm optimization (LPSO) algorithm.

The training process for LFPSO [26] can be applied to identify the most useful features for classification by optimizing feature selection, tuning parameters of machine learning models like SVM or CNN to enhance performance, and improving image preprocessing steps to enhance image quality before feature extraction. By utilizing the exploration capabilities of Levy flight, models for detecting brain tumors may become more accurate and robust using LFPSO.

3.5 Classification using Hybrid Deep learning classification Models with CNN - LSTM

A crucial problem in medical imaging is the diagnosis of brain tumors [27], where precise categorization is essential for patient care and prognosis. A robust hybrid deep learning model that capitalizes on the advantages of both architectures is created by fusing Convolutional Neural Networks (CNNs) with Long Short-Term Memory (LSTM) networks. While LSTMs are excellent at capturing temporal connections, CNNs excel at extracting spatial characteristics. This section explores the hybrid CNN-LSTM model for brain tumor detection, presenting key formulas, equations, and the algorithmic approach.

3.5.1 CNN-LSTM Hybrid Model Architecture

The hybrid model starts with CNNs [28], which are effective at capturing spatial hierarchies through fully connected, pooling, and convolutional layers in images. For an input image X with dimensions $H\times W\times D$ (where L is the depth or number of channels, B is the height, and W is the width), the convolution operation applies a filter $F$of size $f_h \times f_w \times D$ to produce an output feature map Y in equation (10):

$$Y_{i,j,k} = \sum_{h=1}^{f_h} \sum_{w=1}^{f_w} \sum_{d=1}^{D} X_{i+h-1,j+w-1,d} \cdot F_{h,w,d,k} \tag{10}$$

Here, k represents the k k-th filter, and i, j are spatial indices.

To introduce non-linearity, the ReLU is applied element-wise in equation (11):

$$\mathrm{ReLU(x)} = \max(0, x) \tag{11}$$

Equation (12) typically uses max pooling to minimize the spatial dimensions of the feature maps.

$$Y_{i,j,k} = \max(X_{2i-1:2i,2j-1:2j,k}) \tag{12}$$

Long-term dependencies in sequential data are intended to be captured by LSTM networks, a subset of RNN. In addition to three gates the input gate i_t, forget gate f_t, and output gate o_t the LSTM unit has a memory cell c_t that has the cell state stable.

The forget gate operation is defined as:

$$f_t = \sigma(W_f.[h_{t-1}, x_t] + b_f \tag{13}$$

The input gate is defined as:

$$i_t = \sigma(W_i.[h_{t-1}, x_t] + b_i \tag{14}$$

The cell state is updated as follows:

$$c_t = f_t \odot c_{t-1} + i_t \odot \tan h\,(W_c.[h_{t-1}, x_t] + b_c \tag{15}$$

The output gate is defined as:

$$o_t = \sigma(W_o.[h_{t-1}, x_t] + b_o \tag{16}$$

Finally, the hidden state is given by:

$$h_t = o_t \odot \tan(c_t) \tag{17}$$

Here, σ represents weight matrices, the sigmoid activation function, and $\odot$, which stands for element-wise multiplication, W_f, W_i, W_c, W_o and b_f, b_i, b_c, b_o are biases.

The CNN-LSTM hybrid model combines LSTMs' capability in temporal dependency modeling with CNNs' ability to extract spatial features. Feeding the CNN's feature maps into the LSTM network is a common architectural approach.

Given an input MRI image I with dimensions $H\times W\times D$, the process begins with CNN-based feature extraction:

$$F_{cnn} = CNN(I) \tag{18}$$

Here, F_{cnn} represents the feature map extracted by the CNN, which is a 3D tensor. F_{cnn} is then reshaped into a 2D matrix suitable for LSTM input:

$$F_{lstm-in} = reshape(F_{cnn}) \tag{19}$$

The LSTM processes the reshaped features to model temporal dependencies:

$$h_t = LSTM(F_{lstm-in}) \tag{20}$$

Finally, classification is performed using a SoftMax function:

$$y_{pred} = \mathrm{SoftMax}(W_h.h_t + b_h) \tag{21}$$

Where W_h *and* b_h are weights and biases associated with the final fully connected layer, and y_{pred} represents the predicted probabilities for each tumor class.

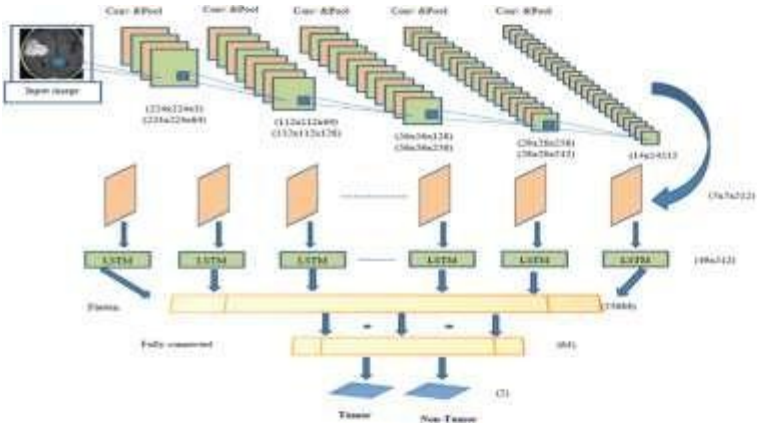

Fig 4 Structure of proposed hybrid CNN-LSTM

CNNs' spatial feature extraction abilities and LSTMs' temporal sequence modeling strengths are successfully combined in the hybrid CNN-LSTM model [29]. Considering the importance of both spatial and contextual information in brain tumor diagnosis, this hybrid technique is especially well-suited.

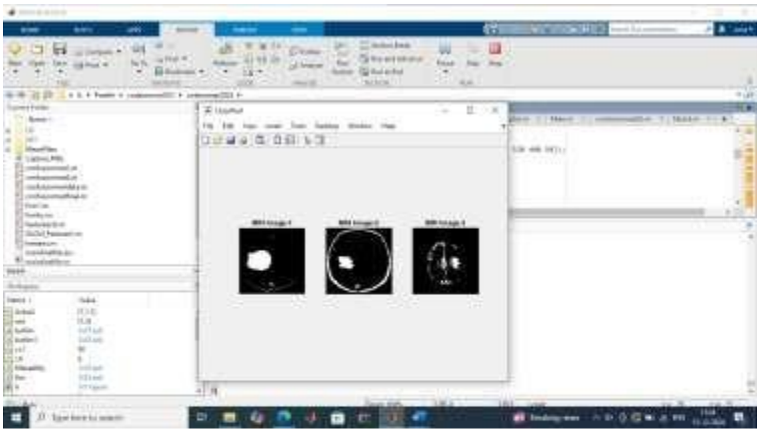

Fig 5. Matlab Implementation Classification Screen

By following the outlined algorithm and utilizing the defined equations, the model can achieve high accuracy in classifying brain tumors from MRI images. Figure 5 and 6 described the classification of images in MATLAB screens. The architecture can be further enhanced by incorporating advanced techniques such as attention mechanisms, transfer learning, or more sophisticated CNN and LSTM architectures.

Fig 6. Final Classified Images in Matlab

EXPERIMENTAL RESULT

In this section [30], we employed the BraTS (Brain Tumor Segmentation) Challenge datasets, which use structural MRI modalities such as T1, T1Gd, T2, and FLAIR particularly for brain tumor analysis. Some versions of these datasets also include Dynamic Contrast-Enhanced MRI (DCE-MRI) sequences, providing additional detail by capturing contrast agent dynamics, which are crucial for characterizing tumor vasculature.

These datasets are meticulously annotated with tumor sub-regions, offering valuable ground truth for training models in tumor detection and classification. Dice score, sensitivity, and specificity were among the performance parameters used to compare the suggested CNN-LSTM hybrid model for brain tumor identification with existing techniques. These metrics provide a comprehensive comparison, ensuring the reliability and accuracy of the developed diagnostic tools.

From the following link the BraTS (Brain Tumor Segmentation) Challenge datasets is collected:

https://www.kaggle.com/datasets/dschettler8845/brats-2021-task1.

These datasets serve as a crucial benchmark for developing advanced brain tumor diagnostic models. A review of the performance comparisons between the current approaches and our suggested CNN-LSTM hybrid model is provided.

To assess the performance of segmentation results, five key parameters are quantified: mean, standard deviation, entropy, kurtosis, and skewness. Each parameter provides different insights into the image characteristics.

Mean

In the context of brain MRI, the average pixel intensity in the image is represented by the mean value. By adding together all of the pixel values and dividing by the total number of pixels, it is computed. Mathematically, this is expressed in equation (22):

$$Mean = \frac{1}{m\times n}\sum_{i=0}^{m-1}\sum_{j=0}^{n-1} I(i,\ j) \quad (22)$$

where $m \ and \ n$ are the image dimensions.

Standard Deviation

In the context of brain MRI, Standard deviation (STD) measures the image's consistency and contrast are reflected in the distribution of pixel values around the mean. It is computed using equation (23) as the variance's square root:

$$\mathrm{STD}(\sigma) = \sqrt{\frac{1}{m\times n}\sum_{i=0}^{m-1}\sum_{j=0}^{n-1}(I(i,j) - M)^2} \quad (23)$$

where M is the mean pixel value.

Entropy

In the context of brain MRI, Entropy quantifies the level of randomness or unpredictability in the image's texture, indicating the amount of information required to describe pixel intensity distribution. Higher entropy values signify a more complex texture, while lower values suggest a more uniform texture in equation (24):

$$Entropy = -\sum_{i=0}^{m-1}\sum_{j=0}^{n-1} f(i,j)\log 2\,(f(i,j)) \quad (24)$$

Kurtosis

In the context of brain MRI, Kurtosis measures the shape of the pixel intensity distribution and the presence of outliers. It helps in understanding the distribution's peakedness or flatness compared to a normal distribution in equation (25):

$$Kurtosis = \frac{\frac{1}{m\times n}\sum_{i=0}^{m-1}\sum_{j=0}^{n-1}(f(i,j)-M)^4}{(STD)^4} \quad (25)$$

where $F(i,j)$ represents pixel intensity and M is the mean.

Skewness

In the context of brain MRI, the asymmetry of the pixel intensity distribution is measured by skewness. It indicates whether the pixel values are more concentrated on one side of the mean in equation (26):

$$Skewness = \frac{\frac{1}{m\times n}\sum_{i=0}^{m-1}\sum_{j=0}^{n-1}(f(i,j)-M)^3}{(STD)^3} \tag{26}$$

where STD is the standard deviation.

Table 1. Performance evaluation of the brain tumor segmentation model

Image types	Mean	STD	Entropy	Kurtosis	Skewness
Meningiomas Tumor Images	0.0051	0.100	3.38	36.32	5.96
Gliomas Tumor Images	0.0050	0.099	3.13	34.23	5.87
Pituitary Tumors Image	0.0052	0.098	3.11	33.12	5.81
Medulloblastomas Tumor Images	0.0051	0.099	3.25	34.75	5.90

Accuracy

In the context of brain MRI [31], the model's total correctness in predicting real pixels is measured by a statistic called accuracy. The percentage of genuine pixels that were accurately anticipated is how it is computed. The equation (21) for accuracy is:

$$Accuracy\ (AC) = \frac{TP+TN}{TP+FP+TN+FN} \tag{21}$$

True positives (TP), true negatives (TN), false positives (FP), and false negatives (FN) would all apply in this scenario.

Table 2. Results of performance comparison

Metrics	Methods						
	KNN	SOM	GA	GCNN	Kernel -Based SVM	ICA-CNN-SVM	DCA-CNN-LSTM
Accuracy	0.85	0.92	0.98	0.96	0.98	0.989	0.991
Sensitivity	0.39	0.43	0.51	0.85	0.98	0.99	0.993
Specificity	0.42	0.52	0.54	0.89	0.98	0.99	0.993
DSC	0.81	0.83	0.85	0.89	0.94	0.981	0.985
Executive Time	3.7s	4.8s	2.8s	0.92s	0.83s	0.43s	0.38s

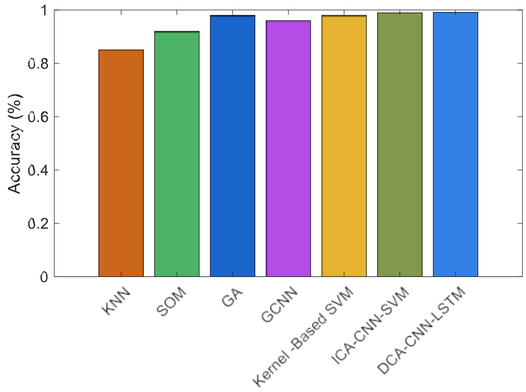

Fig 5 Accuracy

The accuracy of seven models in brain tumor detection is compared in the performance analysis graph shown in Fig. 5. The accuracy of the DCA-CNN-LSTM model is 99.1% followed by ICA-CNN-SVM at 98.9%. GA and Kernel-Based SVM both achieve 98%, while GCNN scores 96%. SOM and KNN lag behind with 92% and 85% accuracy, respectively.

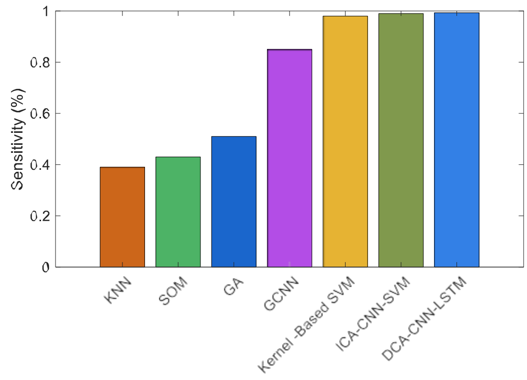

Fig 6 Sensitivity

Sensitivity

In the context of brain MRI [32], sensitivity measures the accuracy in identifying pixels that belong to positive classes. It measures how well a model can identify positive occurrences. Equation (22) defines sensitivity as the proportion of real positive pixels to all pixels that are classified as positive. The True Positive Rate (TPR) is another name for sensitivity. The sensitivity equation is:

$$Sensitivity = \frac{TP}{TP+FN} \tag{22}$$

In fig 6, The sensitivity of seven models the performance analysis graph compares the identification of brain tumors. The DCA-CNN-LSTM model demonstrates the highest sensitivity at 99.3%, closely followed by ICA-CNN-SVM with 99%. Kernel-Based SVM achieves 98%, while GCNN reaches 85%. In contrast, the Genetic Algorithm (GA), Self-Organizing Map (SOM), and K-Nearest Neighbors (KNN) models exhibit lower sensitivity levels, with values of 51%, 43%, and 39%, respectively. This comparison highlights the superior ability of the DCA-CNN-LSTM model to accurately determine brain tumor detection situations that are genuine positives, outperforming the other models.

Specificity

In the context of brain MRI [33], Specificity in brain MRI imaging measures the accuracy in identifying pixels that belong to negative classes. It measures how well a model can identify unfavourable occurrences. According to equation 23, specificity is the ratio of real negative pixels to all pixels that have been recognized as negative. Specificity is also known as the True Negative Rate (TNR). The equation (23) for specificity is:

$$Specificity = \frac{TN}{TN+FP} \tag{23}$$

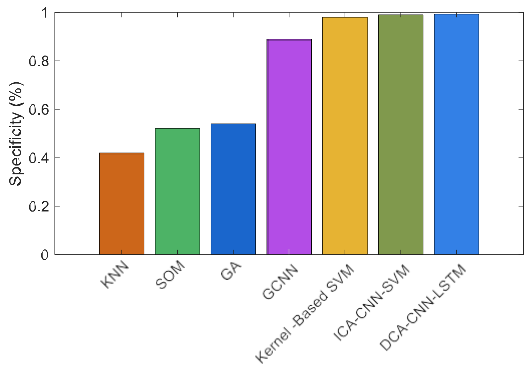

Fig 7 Specificity

From the Fig 7, The specificity of seven models the performance analysis graph assesses the identification of brain tumors. The DCA-CNN-LSTM model achieves the highest specificity at 99.3%, closely followed by ICA-CNN-SVM with 99%. The Kernel-Based SVM model also performs well, reaching 98% specificity, while the GCNN model records a specificity of 89%. In contrast, the Genetic Algorithm (GA), Self-Organizing Map (SOM), and K-Nearest Neighbors (KNN) models show lower specificity levels, with values of 54%, 52%, and

42%, respectively. This comparison underscores the DCA-CNN-LSTM model's superior capability to accurately identify true negative cases in brain tumor detection, significantly outperforming the other models.

Dice Similarity Coefficient (DSC)

In brain MRI [34], the overlap between the actual ground truth and the projected output is measured by the Dice Similarity Coefficient (DSC). It calculates the degree of similarity between the ground truth and anticipated areas. The true positive values and the mean of the ground truth and anticipated values are compared to determine the dice score. The Dice score's equation (24) is as follows:

$$DSC = \frac{2 \times TP}{2 \times TP + FN + FP} \tag{24}$$

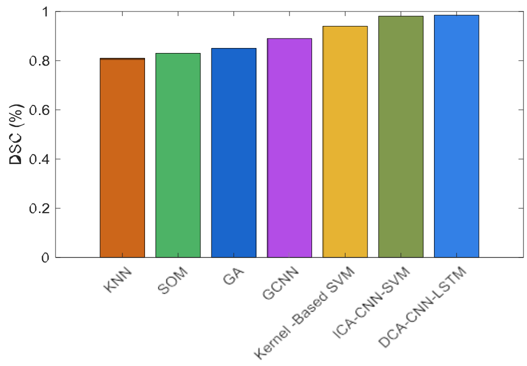

Fig 8 Dice Similarity Coefficient (DSC)

Figure 8 shows the performance analysis graph evaluating the Dice Similarity Coefficient (DSC) of seven models for brain tumor identification. The model with the highest DSC of 0.993 is the DCA-CNN-LSTM model, indicating excellent alignment between predicted and actual tumor regions. The ICA-CNN-SVM model follows closely with a DSC of 0.99, and the Kernel-Based SVM model achieves a DSC of 0.98. The GCNN model also performs well with a DSC of 0.89. In contrast, the Genetic Algorithm (GA), Self-Organizing Map (SOM), and K-Nearest Neighbors (KNN) models exhibit lower DSC values of 0.54, 0.52, and 0.42, respectively. This comparison highlights the DCA-CNN-LSTM model's superior ability in accurately segmenting brain tumors, outperforming the other models by a significant margin.

Execution Time

In the context of brain MRI [35], To assess the efficiency of the model, execution time is crucial. It represents the duration required for the model to process an image and produce a result. Execution time can be measured in seconds or milliseconds and provides insight into the computational performance of the model.

In practice, execution time T can be calculated using the equation (25):

$$\mathrm{T} = End\ Time - Start\ Time \tag{25}$$

where the End Time and Start Time are the timestamps recorded at the end and start of the model's processing phase, respectively. This metric helps in evaluating accuracy and computational efficiency trade-off in brain tumor detection tasks.

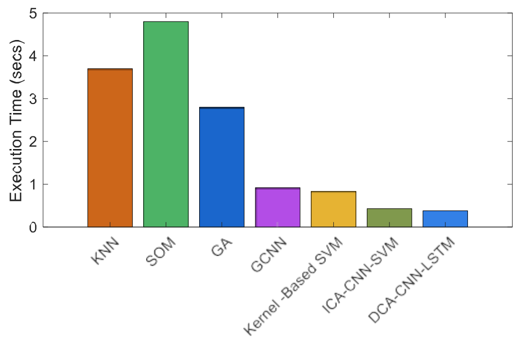

Fig 8 Execution Time

From the fig 8, In assessing the execution times for different brain tumor detection models, the DCA-CNN-LSTM model is the most efficient, with a processing time of just 0.38 seconds. It is followed by the ICA-CNN-SVM model, which has an execution time of 0.43 seconds. The Kernel-Based SVM model has a slightly longer execution time of 0.83 seconds, while the GCNN model takes 0.92 seconds. Conversely, the KNN and SOM models show significantly longer execution times of 3.7 and 4.8 seconds, respectively. The GA model's execution times vary between 2.8 and 5 seconds, indicating greater variability and slower processing compared to the other models. Overall, the DCA-CNN-LSTM model excels not only in accuracy but also in processing speed.

CONCLUSION

In conclusion, this research proposed an innovative brain tumor detection framework that merges advanced preprocessing techniques with a hybrid deep learning approach. By employing Dynamic Contrast-Enhanced MRI (DCE-MRI) alongside adaptive multi-scale Gaussian filtering, the method significantly enhances image quality and minimizes noise. RFECV is used for precise feature selection, complemented by Levy Flight Particle Swarm Optimization (LFPSO) for comprehensive feature extraction. The integration of CNNs with Long Short-Term Memory (LSTM) networks captures both spatial and temporal patterns, resulting in exceptional classification accuracy. The method achieves impressive performance metricsn 0.991 accuracy, 0.993 sensitivity and specificity, and a Dice Similarity Coefficient of 0.985 while maintaining an efficient processing time of 0.38 seconds. This advanced framework demonstrates significant potential for enhancing brain tumor detection, offering a more accurate and efficient solution that could greatly benefit patient outcomes in clinical practice.

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